In the Specification:

Please amend the first paragraph under the subtitle "Related Applications" to read as follows:

--This application is a divisional application of U.S. Serial No. 09/438,016, filed November 10, 1999 (allowed February 16, 2001), which claims priority under 35 U.S.C. §119(e) to U.S. Patent Application Serial No. 60/107,986, filed November 10, 1998, and to Application Serial No. 60/140,785, filed June 23, 1999, the entire disclosures of which are incorporated herein by reference.--

In the Claims:

Please cancel claims 1-30 and 32-47 as filed in the parent application upon which priority for this application is claimed.

REMARKS

Claim 31 is pending in this application. Claims 1-30 and 32-47 have been canceled.

Attached hereto is a page showing all the claims as currently pending, which is entitled "**Pending Claims**."

The Commissioner is hereby authorized to credit any overpayment or charge any additional fees in connection with the filing of this Preliminary Amendment to our Deposit Account No. 50-1181.

Respectfully submitted,
GENSET CORPORATION

Date: 14 May 01, 2001

By: [signature]
John Lucas, Ph.D., J.D.
Registration No. 43,373

10665 Sorrento Valley Road
San Diego, CA 92121-1609
Telephone: (858) 597-2600
Facsimile: (858) 597-2601
e-mail: john.lucas@genxy.com

Certificate of Mailing under 37 CFR 1.10

Express Mail Label No.: EL821903728US
Date of Deposit: May ~~14~~ 15, 2001

I hereby certify that this correspondence is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10, on the Date of Deposit shown above, postage prepaid and is addressed to the Commissioner of Patents and Trademarks, Washington, D.C. 20231.

[signature]
Signature

C M McClure
Typed or Printed Name of Person Signing Certificate

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Claims 1-30 have been canceled.

31. (Amended) A method of determining whether a candidate genomic region harbors a gene associated with a detectable trait comprising determining whether the association of a plurality of biallelic markers located in said candidate genomic region with said detectable trait is significantly different than the association of a plurality of biallelic markers located in a plurality of random genomic regions [wherein the determination of whether the association of said plurality of biallelic markers located in said candidate genomic region with said detectable trait is significantly different than the association of said plurality of biallelic markers located in a plurality of random genomic regions comprises:

constructing a candidate region distribution of test values using said biallelic markers in said candidate genomic region, said candidate region distribution of test values being indicative of the difference in the haplotype frequencies of said biallelic markers in said candidate region in individuals who possess said detectable trait and control individuals who do not possess said detectable trait;

constructing a random region distribution of test values using said biallelic markers in said genomic region said random region distribution of test values being indicative of the difference in the haplotype frequencies of said biallelic markers in said random genomic regions in individuals who possess said detectable trait and control individuals who do not possess said detectable trait; and

comparing said candidate region distribution of test values with said random region distribution of test values.]

Claims 32-47 have been canceled.

Claims as Pending after Preliminary Amendment

31. A method of determining whether a candidate genomic region harbors a gene associated with a detectable trait comprising determining whether the association of a plurality of biallelic markers located in said candidate genomic region with said detectable trait is significantly different than the association of a plurality of biallelic markers located in a plurality of random genomic regions.